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Analysis Of Nucleotide Diversity In ***Coffea*** spp.

Luiz Filipe P Pereira[1,2] , Karina Yanagui[2] , Lucia P Ferreira[2] , Douglas S Domingues[2] , Luiz G E Vieira[2] , David Pot[1,3]

[1] Embrapa Café,PqEB s/n, Brasília, DF,70770-901, Brasil
[2] Lab. Biotecnologia, IAPAR, Rod. Celso Garcia CID Km 375, Londrina, PR, 86001-970, Brasil
[3] CIRAD, Avenue Agropolis, TA-A-96/03, 34398 Montpellier Cedex, France

Marker-assisted selection becomes a reality for many crops; in perennial crops, the utilization of molecular markers in breeding programs can speed up genotype selection. However, the most important commercial coffee species - allotetraploid *C. arabica* - has a restrict number of available polymorphic markers, which is a consequence of the narrow genetic basis and low molecular variability among cultivars. In order to study the nucleotide diversity in *C. arabica*, as well in other diploid *Coffea* relatives, we sequenced PCR amplified fragments of nine genes in 20 *Coffea* genotypes: twelve *C. arabica*, including eight wild genotypes and four commercial cultivars; and eight *C. canephora* genotypes. Genotypes of *C. eugenioides*, *C. racemosa* and *Psylanthus bengalensis* were also included in this analysis. From a total of 9 Kb analyzed, we found 573 polymorphisms: 500 SNPs; 39 INDELs and 34 SSRs. In *C. canephora* genotypes, we detected 188 polymorphisms (frequency of 2.09/100bp). For *C. arabica* we obtained similar results: 144 polymorphism (frequency of 2.13/100bp). Most of the polymorphism found in *C. arabica* only reflected the differences between ancestral homeologs, and they were monomorphic among different genotypes. However, 19 % of these polymorphisms (27 SNPs) were interespecific for *C. arabica*, and 13 of them were fixed among genotypes. The strategy of this work reflects the importance in using a more diverse panel of genotypes in order to identify SNPs in *C. arabica*, pointing out that the exploitation of wild germplasm will be an important source of genetic variability.